```
=> d his

     (FILE 'HOME' ENTERED AT 07:25:19 ON 09 MAY 2001)

     INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS,
     BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT,
     CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE,
     DRUGB, DRUGLAUNCH, DRUGMONOG2, DRUGNL, ...' ENTERED AT 07:25:29 ON 09 MAY
     2001
               SEA SEQUENCING AND HYBRIDIZATION AND UNIVERSAL AND NUCLEOTIDE A
               ---------
                 1   FILE BIOSIS
                 1   FILE CABA
                 1   FILE LIFESCI
                 1   FILE MEDLINE
                 1   FILE PROMT
              1415   FILE USPATFULL
L1               QUE SEQUENCING AND HYBRIDIZATION AND UNIVERSAL AND NUCLEOTIDE A
               ---------

     FILE 'BIOSIS, CABA, LIFESCI, MEDLINE, PROMT' ENTERED AT 07:27:29 ON 09
     MAY 2001
L2             5 S L1
L3             4 DUP REM L2 (1 DUPLICATE REMOVED)

     INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS,
     BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT,
     CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE,
     DRUGB, DRUGLAUNCH, DRUGMONOG2, DRUGNL, ...' ENTERED AT 07:27:58 ON 09 MAY
     2001
               SEA SEQUENCING AND HYBRIDIZATION AND ITERATIVE AND PATTERN AND
               ---------
                 1   FILE MEDLINE
               140   FILE USPATFULL
L4               QUE SEQUENCING AND HYBRIDIZATION AND ITERATIVE AND PATTERN AND
               ---------

     FILE 'MEDLINE' ENTERED AT 07:29:41 ON 09 MAY 2001
L5             1 S L4

     INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS,
     BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT,
     CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE,
     DRUGB, DRUGLAUNCH, DRUGMONOG2, DRUGNL, ...' ENTERED AT 07:30:03 ON 09 MAY
     2001
               SEA SEQUENCING AND HYBRIDIZATION AND ITERATIVE AND (POLYNUCLEOT
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                 1   FILE BIOSIS
                 3   FILE MEDLINE
                 2   FILE PROMT
               289   FILE USPATFULL
                 1   FILE WPIDS
                 1   FILE WPINDEX
L6               QUE SEQUENCING AND HYBRIDIZATION AND ITERATIVE AND (POLYNUCLEOT
               ---------

     FILE 'BIOSIS, MEDLINE, PROMT, WPIDS' ENTERED AT 07:33:05 ON 09 MAY 2001
L7             7 S L6
L8             7 DUP REM L7 (0 DUPLICATES REMOVED)

     FILE 'STNGUIDE' ENTERED AT 07:34:05 ON 09 MAY 2001
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      INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, ANABSTR, AQUA[illegible] BIOBUSINESS,
      BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, C[illegible]A, CANCERLIT,
      CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE,
      DRUGB, DRUGLAUNCH, DRUGMONOG2, DRUGNL, ...' ENTERED AT 07:35:34 ON 09 MAY
      2001
                 SEA ITERATIVE AND UNIVERSAL AND DESIGNATE AND (PROBE# OR OLIGON
                ---------
                5    FILE USPATFULL
                1    FILE WPIDS
                1    FILE WPINDEX
L9               QUE ITERATIVE AND UNIVERSAL AND DESIGNATE AND (PROBE# OR OLIGON
                ---------
                 SEA ITERATIVE AND UNIVERSAL AND DESIGNATE AND (PROBE# OR OLIGON
                ---------
                3    FILE DGENE
               10    FILE USPATFULL
                1    FILE WPIDS
                1    FILE WPINDEX
L10              QUE ITERATIVE AND UNIVERSAL AND DESIGNATE AND (PROBE# OR OLIGON
                ---------

      FILE 'USPATFULL, DGENE, WPIDS' ENTERED AT 07:38:19 ON 09 MAY 2001
L11           14 S L10

      FILE 'STNGUIDE' ENTERED AT 07:39:01 ON 09 MAY 2001

=> log y

COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.00      68.28

STN INTERNATIONAL LOGOFF AT 07:41:37 ON 09 MAY 2001
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L7 ANSWER 22 OF 27 JICST-EPlus COPYRIGHT 2001 JST
ACCESSION NUMBER: 980017823 JICST-EPlus
TITLE: Investigation for establishing an efficient DNA sequence analysis by hybridization with stacking **probe**.
AUTHOR: HATAKEYAMA KAZUHISA; KATO YUKIE; KUWAHARA KOICHIRO; ASAI YOKO; TERASAWA MASATO; YUKAWA HIDEAKI
CORPORATE SOURCE: Mitsubishi Chemical Corp.
SOURCE: Baiotekunoroji Shinpojiumu Yokoshu, (1997) vol. 15th, pp. 189-195. Journal Code: L0180A (Fig. 3, Ref. 8)
PUB. COUNTRY: Japan
DOCUMENT TYPE: Conference; Short Communication
LANGUAGE: Japanese
STATUS: New

AB Sequencing by hybridization(SBH), based on the ability to determine a DNA sequence by hybridizing **oligonucleotide** probes to the target DNA, appears to be a method with great potential for megabase sequencing. The target DNA sequence can be determined by assembling the sequences of those oligonucleotides that perfectly match the target DNA. One of the technical hurdles of this method is that SBH requires extremely highly specific hybridization conditions that enable to discriminate imperfectly matched from perfectly matched duplexes. In this report, we propose new **probe** designs that contain several **universal bases**, such as inosine or 5-nitroindole, at both ends. By using these probes, we could obtain not only strong hybridization signals, but also high discrimination values. Particularly, single end mismatched duplexes, the most stable of the imperfectly matched duplexes, could reproducibly be discriminated. Introduction: SBH has been proposed as a low cost and high throughput sequencing method which could potentially determine megabase DNA sequences. Though the potential of SBH is attractive, there are several technical hurdles that prevent its practical use. One of the most serious problems is that SBH requires extremely highly specific hybridization conditions which can discriminate one-base mismatches against a perfect match. Despite reports of hybridization conditions which allow to discriminate one-base mismatches in **oligonucleotide** probes and despite several SBH model experiments, the attained discrimination values are to date not yet suitable to determine long sequences. Determination of sequences of a long DNA fragment particularly requires optimal hybridization conditions, as with these fragments, probes have higher probabilities to hybridize to imperfectly matched targets, which results in false positive data. (author abst.)

L7 ANSWER 20 OF 27 JICST-EPlus COPYRIGHT 2001 JST
ACCESSION NUMBER: 990584121 JICST-EPlus
TITLE: Highthroughput gene analysis by hybridization with DNA arrays.
AUTHOR: HATAKEYAMA KAZUHISA; KUWAHARA KOICHIRO; MOTTAGUI-TABAR S; KOBAYASHI KAN; TERASAWA MASATO
CORPORATE SOURCE: Mitsubishi Chemical Corp.
SOURCE: Baiotekunoroji Shinpojiumu Yokoshu, (1998) vol. 16th, pp. 192-197. Journal Code: L0180A (Fig. 2, Ref. 5)
PUB. COUNTRY: Japan
DOCUMENT TYPE: Conference; Article
LANGUAGE: Japanese
STATUS: New

AB Proceedings of DNA array technology opened the way for the high throughput gene analysis, such as sequence analysis by hybridization(SBH) or gene expression monitoring. SBH, based on the ability to determine a DNA sequence by hybridizing **oligonucleotide** probes to the target DNA, appears to be a method with great potential for megabase sequencing. The target DNA sequence can be determined by assembling the sequences of those oligonucleotides that perfectly match the target DNA. One of the technical hurdles of this method is that SBH requires extremely highly specific hybridization conditions that enable to discriminate imperfectly matched from perfectly matched duplexes. In this report, we propose new **probe** designs that contain several **universal bases**, such as inosine or 5-nitroindole, at both ends. By using these probes, we could obtain not only strong hybridization signals, but also high discrimination values. Particularly, single end mismatched duplexes, the most stable of the imperfectly matched duplexes, could reproducibly be discriminated. (author abst.)

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     FILE 'CAPLUS, SCISEARCH, EMBASE, ESBIOBASE, MEDICONF, BIOTECHNO' ENTERED
     AT 15:42:50 ON 17 MAY 2001
L3           20 S UNIVERSAL (W) BASES/TI
L4            9 DUP REM L3 (11 DUPLICATES REMOVED)

     INDEX '1MOBILITY, 2MOBILITY, ADISALERTS, AEROSPACE, AGRICOLA, ALUMINIUM,
     ANABSTR, AQUASCI, BABS, BIBLIODATA, BIOBUSINESS, BIOCOMMERCE, BIOSIS,
     BIOTECHABS, BIOTECHDS, BIOTECHNO, BLLDB, CABA, CANCERLIT, CAPLUS, CBNB,
     CEABA-VTB, CEN, CERAB, CHEMSAFE, CIN, ...' ENTERED AT 15:44:50 ON 17 MAY
     2001
               SEA UNIVERSAL (W) BASES AND (POLYNUCLEOTIDE OR OLIGONUCLEOTIDE
              ---------
              6   FILE BIOSIS
              2   FILE BIOTECHABS
              2   FILE BIOTECHDS
              5   FILE BIOTECHNO
              6   FILE CAPLUS
              2   FILE COMPENDEX
              2   FILE COMPUAB
             76   FILE DGENE
              5   FILE EMBASE
              2   FILE ENERGY
              4   FILE ESBIOBASE
              6   FILE EUROPATFULL
              3   FILE IFIPAT
              2   FILE JICST-EPLUS
              3   FILE LIFESCI
              5   FILE MEDLINE
             72   FILE PCTFULL
              1   FILE PROMT
              4   FILE SCISEARCH
              2   FILE TOXLIT
             37   FILE USPATFULL
              5   FILE WPIDS
              5   FILE WPINDEX
L5             QUE UNIVERSAL (W) BASES AND (POLYNUCLEOTIDE OR OLIGONUCLEOTIDE
              ---------

     FILE 'BIOSIS, CAPLUS, EUROPATFULL, BIOTECHNO, EMBASE, MEDLINE, WPIDS,
     ESBIOBASE, SCISEARCH, IFIPAT, LIFESCI, BIOTECHDS, COMPENDEX, COMPUAB,
     ENERGY, JICST-EPLUS, TOXLIT, PROMT' ENTERED AT 15:47:14 ON 17 MAY 2001
L6           65 S L5
L7           27 DUP REM L6 (38 DUPLICATES REMOVED)

=> log y

COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                    75.55     112.07

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)          SINCE FILE      TOTAL
                                                       ENTRY    SESSION
CA SUBSCRIBER PRICE                                    -0.59      -3.53

STN INTERNATIONAL LOGOFF AT 15:57:04 ON 17 MAY 2001
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L3 ANSWER 1 OF 4 MEDLINE
ACCESSION NUMBER: 2000047397 MEDLINE
DOCUMENT NUMBER: 20047397 PubMed ID: 10582572
TITLE: Optimal reconstruction of a sequence from its probes.
AUTHOR: Frieze A M; Preparata F P; Upfal E
CORPORATE SOURCE: Department of Mathematical Sciences, Carnegie Mellon University, Pittsburgh, PA 15213, USA.. aflp@andrew.cmu.edu
SOURCE: JOURNAL OF COMPUTATIONAL BIOLOGY, (1999 Fall-Winter) 6 (3-4) 361-8.
Journal code: CGW; 9433358. ISSN: 1066-5277.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199912
ENTRY DATE: Entered STN: 20000114
Last Updated on STN: 20000114
Entered Medline: 19991230

AB An important combinatorial problem, motivated by DNA **sequencing** in molecular biology, is the reconstruction of a sequence over a small finite alphabet from the collection of its probes (the sequence spectrum), obtained by sliding a fixed sampling pattern over the sequence. Such construction is required for **Sequencing**-by-**Hybridization** (SBH), a novel DNA **sequencing** technique based on an array (SBH **chip**) of short **nucleotide** sequences (probes). Once the sequence spectrum is biochemically obtained, a combinatorial method is used to reconstruct the DNA sequence from its spectrum. Since technology limits the number of probes on the SBH **chip**, a challenging combinatorial question is the design of a smallest set of probes that can sequence an arbitrary DNA string of a given length. We present in this work a novel probe design, crucially based on the use of **universal** bases [bases that bind to any **nucleotide** (Loakes and Brown, 1994)] that drastically improves the performance of the SBH process and asymptotically approaches the information-theoretic bound up to a constant factor. Furthermore, the **sequencing** algorithm we propose is substantially simpler than the Eulerian path method used in previous solutions of this problem.